

Figure 1(a)-1

1 CCTCTCTGTTTCGTTCCGTAGACGAAGAAGAAGAAGAAATCTCA  
46 GGTTTTAGCTTTTCGAAGCTTCCAAAATTTTGAATTTTGATCTTCT  
91 GGGCTCTTTTGTAATCAGACTGAAGATATTTAGATTACCCAGAA  
136 GTTGTTCAAGGAATGGTTTCAGTGGACAGCACGGAAGATATAAAG  
181 AGACTTTTTTTCCAGATTTTGCTGATCCAAAATCTGAATAGTTG  
226 TTCATGTTCTTTGGATCAAATCTGGAAGAGGAAGTTGTTGGATC  
271 TAGAAGAAGATAACAATGTTGGATTCTCTAGTGTGCGAAACTGCCT  
M L D S L V S K L P 10  
316 TCGTTATCGACATCTGATCACGCTTCTGTGGTTGCGTTGAATCTC  
S L S T S D H A S V V A L N L 25  
361 TTTGTGCACTTTCTTTGTGCTTGATTGTTCTTTGGTCACTTTTG  
F V A L L C A C I V L G H L L 40  
406 GAAGAGAATAGATGGATGAACGAATCCATCACC GCCTTGTGATT  
E E N R W M N E S I T A L L I 55  
451 GGGCTAGGCACTGGTGTTACCATTTTGTGATTAGTAAAGGAAAA  
G L G T G V T I L L I S K G K 70  
496 AGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATAT  
S S H L L V F S E D L F F I Y 85  
541 CTTTTGCCACCCATTATATTC AATCGAGGGTTTCAAGTAAAAAG  
L L P P I I F N A G F Q V K K 100  
586 AAGCAGTTTTTCCGCAATTTCTGTGACTATTATGCTTTTTGGTGCT  
K Q F F R N F V T I M L F G A 115  
631 GTTGGGACTATTATTTCTTG CACAATCATATCTCTAGGTGTAACA  
V G T I I S C T I I S L G V T 130  
676 CAGTTCTTTAAGAAGTTGGACATTGGAACCTTTGACTTGGGTGAT  
Q F F K K L D I G T F D L G D 145  
721 TATCTTGCTATTGGTGCCATATTTGCTGCAACAGATT CAGTATGT  
Y L A I G A I F A A T D S V C 160  
766 ACACTGCAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGT  
T L Q V L N Q D E T P L L Y S 175  
811 CTTGTATTCGGAGAGGGTGTGTAATGATGCAACGTCAGTTGTC  
L V F G E G V V N D A T S V V 190  
856 GTCTTCAACGCGATT CAGAGCTTTGATCTCACTCACCTAAACCAC  
V F N A I Q S F D L T H L N H 205  
901 GAAGCTGCTTTTCTCTCTTGGAACTTCTGTATTTGTTTCTC  
E A A F H L L G N F L Y L F L 220  
946 CTAAGTACCTTGCTTGGTGCTGCAACCGGTCTGATAAGTGCGTAT



Figure 1(a)-2

991 L S T L L G A A T G L I S A Y 235  
GTTATCAAGAAGCTATACTTTGGAAGGCACTCAACTGACCGAGAG  
V I K K L Y F G R H S T D R E 250  
1036 GTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGCT  
V A L M M L M A Y L S Y M L A 265  
1081 GAGCTTTTCGACTTGAGCGGTATCCTCACTGTGTTTTCTGTGGT  
E L F D L S G I L T V F F C G 280  
1126 ATTGTGATGTCCCATTAACACATGGCACAATGTAACGGAGAGCTCA  
I V M S H Y T W H N V T E S S 295  
1171 AGAATAACAACAAAGCATACCTTTGCAACTTTGTCAATTTCTTGCG  
R I T T K H T F A T L S F L A 310  
1216 GAGACATTTATTTCTTGATGTTGGAATGGATGCCTTGGACATT  
E T F I F L Y V G M D A L D I 325  
1261 GACAAGTGAGATCCGTGAGTGACACACCGGAACATCGATCGCA  
D K W R S V S D T P G T S I A 340  
1306 GTGAGCTCAATCCTAATGGGTCTGGTCATGTTGGAGAGACAGCG  
V S S I L M G L V M V G R A A 355  
1351 TTCGTCTTTCCGTTATCGTTTCTATCTAACTAGCCAAGAAGAAT  
F V F P L S F L S N L A K K N 370  
1396 CAAAGCGAGAAAAATCAACTTTAACATGCAGGTTGTGATTGGTG  
Q S E K I N F N M Q V V I W W 385  
1441 TCTGGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGACATAAC  
S G L M R G A V S M A L A Y N 400  
1486 AAGTTTACAAGGGCCGGGCACACAGATGTACGCGGAATGCAATC  
K F T R A G H T D V R G N A I 415  
1531 ATGATCACGAGTACGATAACTGTCTGTCTTTTAGCACAGTGGTG  
M I T S T I T V C L F S T V V 430  
1576 TTTGGTATGCTGACCAAACCACTCATAAGTACCTATTACCGCAC  
F G M L T K P L I S Y L L P H 445  
1621 CAGAACGCCACCACGAGCATGTTATCTGATGACAACCCCCAAA  
Q N A T T S M L S D D N T P K 460  
1666 TCCATACATATCCCTTTGTTGGACCAAGACTCGTTTCATTGAGCCT  
S I H I P L L D Q D S F I E P 475  
1711 TCAGGGAACCACAATGTGCCTCGGCCTGACAGTATACGTGGCTTC  
S G N H N V P R P D S I R G F 490  
1756 TTGACACGGCCCATCGAACCCTGCATTACTGAGACAAATTT  
L T R P T R T V H Y Y W R Q F 505





Figure 1(a)-3

1801 GATGACTCCTTCATGCGACCCGCTTTGGAGGTCGTGGCTTTGTA  
D D S F M R P V F G G R G F V 520  
1846 CCCTTTGTTCCAGGTTCTCCAAGTGAAGAGAAACCTCCTGATCTT  
P F V P G S P T E R N P P D L 535  
1891 AGTAAGGCTTGAGGGTAACGTGGAAGAAAAGCTTTGATTTTTTTT  
S K A 538  
1936 GGTAAGAAAGGGTGATTCAAATTATGCTTTTGTGTAAATTATCCA  
1981 TTTGTAATATTGTTTGTGAGGACAGAAATCTGTCCTAACGTTTTG  
2026 AGAGCAGAAAGCAAAACATGGCAACTTTGAAGTGTTGATTGATG  
2071 TATGTAATTATATTCATATTTGTTTTGTTGTAACACAACTACAC  
2116 ATTTGTTTATGTTTGAATTTGGTTTTTGCTTCGAAAAAAAAAAAA  
2161 AAAAAAAAAAAAAAAAAA

Figure 1(b)-1



1	TCTTCGTTTGCATTGGTGTTTTCAAATCGACGAAATCGAAAA	
46	ATTATCGAGTGAAAAATGAGTATCGGATTAACAGAGTTTGTGACG	
	M S I G L T E F V T	10
91	AATAAACTAGCAGCTGAGCATCCTCAGGTATACCAATCTCAGTG	
	N K L A A E H P Q V I P I S V	25
	TTCATCGCCATTCTCTGTCTATGTTAGTTATCGGCCACTTGCTT	
46	F I A I L C L C L V I G H L L	40
181	GAAGAGAATCGATGGGTAAATGAATCTATTACCGCCATTTTAGTA	
	E E N R W V N E S I T A I L V	55
226	GGAGCAGCATCAGGAACAGTGATCTTACTTATTAGTAAAGGAAAA	
	G A A S G T V I L L I S K G K	70
271	AGTTACACATATTTTGGTGTGTGATGAAGAAGTCTTCTTCATTAC	
	S S H I L V F D E E L F F I Y	85
316	CTTCTTCTCCATAATCTTCAATGCTGGGTCCAGTTAAGAAA	
	L L P P I I F N A G F Q V K K	100
361	AAGAAGTTTTTTCACAACCTTTTTAACCATCATGTCCTTTGGTGTG	
	K K F F H N F L T I M S F G V	115
406	ATTGGAGTTTTTCATCTCCACTGTCAATTATCTCGTTTGGGACTTGG	
	I G V F I S T V I I S F G T W	130
451	TGGCTGTTTCCCAAGTTGGGATTTAAGGGGTTGAGTGCTAGAGAC	
	W L F P K L G F K G L S A R D	145
496	TATCTTGCCATAGGAACGATTTTCTCATCAACTGATACTGTTTGC	
	Y L A I G T I F S S T D T V C	160
541	ACTCTACAGATTCTCCATCAAGATGAAACACCATTGCTATACAGC	
	T L Q I L H Q D E T P L L Y S	185
586	TTAGTCTTTGGAGAAGGAGTGGTGAATGATGCAACCTCAGTTGTA	
	L V F G E G V V N D A T S V V	195
631	CTGTTCAACGCCGTGCAAAAGATTCAATTTGAAAGCCTAACCGGT	
	L F N A V Q K I Q F E S L T G	205
676	TGGACGGCGCTGCAAGTATTTGGGAACCTTTTGTACCTCTTCTCA	
	W T A L Q V F G N F L Y L F S	220
721	ACAAGCACACTTCTCGGAATTGGTGTGGGGCTAATAACATCTTTT	
	T S T L L G I G V G L I T S F	235
766	GTTCTTAAACCTTGTATTTTGAAGACATTCTACTACACGCGAA	
	V L K T L Y F G R H S T T R E	250
811	CTCGCCATCATGGTTCTAATGGCTTACCTTTTCATATATGTTGGCT	
	L A I M V L M A Y L S Y M L A	265

Figure 1(b)-2

856 GAGCTCTTCTCATTAAAGTGAATTCTTACTGTTTTCTTCTGTGGT 280  
E L F S L S G I L T V F F C G  
901 GTTTTAATGTCGCATTATGCATCATATAACGTGACAGAGAGCTCA 295  
V L M S H Y A S Y N V T E S S  
946 AGAATCACTTCCAGGCATGTATTGCAATGTTGTCCTTTATTGCG 310  
R I T S R H V F A M L S F I A  
991 GAGACATTCATATTTCTGTATGTTGGAACAGATGCTCTTGATTTT 325  
E T F I F L Y V G T D A L D F  
1036 ACAAAGTGAAGACAAGCAGCTTAAGCTTTGGGGTACTCTGGGT 340  
T K W K T S S L S F G G T L G  
1081 GTCTCCGGTGTCAACCGCATTAGTATTGCTTGGACGAGCAGCA 355  
V S G V I T A L V L L G R A A  
1126 TTTGTCTTTCCACTCTCGGTCTTAACAAATTCATGAACAGGCAC 370  
F V F P L S V L T N F M N R H  
1171 ACTGAAAGAAACGAGTCTATCACATTTAAGCATCAGGTGATCATT 385  
T E R N E S I T F K H Q V I I  
1216 TGGTGGGCAGGTCTAATGCGAGGTGCTGTCTCAATTGCTCTGGCT 400  
W W A G L M R G A V S I A L A  
1261 TTCAAGCAGTTCACATACTCCGGTGTTACATTGGATCCTGTGAAT 415  
F K Q F T Y S G V T L D P V N  
1306 GCTGCCATGGTCACCAACACCCTATCGTTGTTCTCTTTACTACA 430  
A A M V T N T T I V V L F T T  
1351 CTGGTCTTTGGTTTCCTCACAAACCACTTGTAATTATCTCCTT 445  
L V F G F L T K P L V N Y L L  
1396 CCTCAAGATGCAAGTCACAACACCGGAAATAGAGGTAACCGCACT 460  
P Q D A S H N T G N R G K R T  
1441 GAGCCAGGTTCTCCGAAAGAAGATGCGACACTTCTCTCTTTCC 475  
E P G S P K E D A T L P L L S  
1486 TTTGACGAGTCTGCTTCCACCAACTTCAATAGAGCTAGAGATAGT 490  
F D E S A S T N F N R A R D S  
1531 ATTTCCCTTCTGATGGAACAACCTGTGTACACCATCCACCGCTAC 505  
I S L L M E Q P V Y T I H R Y  
1576 TGGAGAAAGTTTGACGACACATACATGAGGCCTATCTTCGGTGGA 520  
W R K F D D T Y M R P I F G G  
1621 CCTCGTCGAGAAAACCAACCAGAATGCTAGAATTGATCCGGGTTTC 529  
P R R E N Q P E C  
1666 TCCGCGGGGAAATCATGATGAGTTAGTTTTTTTTTATAGTCAAGAA



Title: GENETIC ENGINEERING SALT  
TOLERANCE IN CROP PLANTS  
Inventor: Eduardo BLUMWALD et al.  
Application No.: 09/271,584

Sheet 6 of 28

Figure 1(b)-3



1711 AGTAGGATAGTTGGTTTAGCTAAAACAGTTTCTTAAAGTTTTGT  
1756 TAAATGTATACAACAAGGTTCTTCTATATACGC

Figure 1 (c)-1



(i)

1 AAAAAAGCTGGAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAG  
46 TGGATCCCCCGGCTGCAGGAATTCGCGGCCGCTCGGCCATGTC  
R A A G I R G R L G H V 12  
91 CTCCGCCGTCATCGATTCCACTATCTTCCTGAAGCCAGCGGTTCG  
L R R H R F H Y L P E A S G S 27  
136 CTTCTCATTGGTTTAATCGTCGGTATACTTGCTAATATCTCCGAC  
L L I G L I V G I L A N I S D 42  
181 ACTGAGACTAGCATTAGGACGTGGTTTAATTTCCACGAAGAGTTC  
T E T S I R T W F N F H E E F 57  
226 TTCTTCTTGTTTTGTTGCCTCCCATCATATTCCAGTCAGGTTTC  
F F L F L P P I I F Q S G F 72  
271 AGTCTTCAACCTAAACCATTTCTTTCTAACTTTGGAGCCATTGTT  
S L Q P K P F F S N F G A I V 87  
316 ACCTTTGCTATCATCGGAACCTTTTGTCGCTTCAGTTGTTACTGGT  
T F A I I G T F V A S V V T G 102  
361 GGTCTGGTTTATCTTGGCGGCTCTATGTATCTCATGTATAAACTT  
G L V Y L G G S M Y L M Y K L 117  
406 CCCTTTGTTGAGTGCTTTATGTTTGGTGCCTTATATCAGCTACG  
P F V E C L M F G A L I S A T 132  
451 GACCTGTCACTGTACTCTCTATATTTCCAGGATGTGGGCACCGAT  
D P V T V L S I F Q D V G T D 147  
496 GTTAACCTGTATGCTTTGGTCTTTGGAGAATCAGTTCTGAATGAT  
V N L Y A L V F G E S V L N D 162  
541 GCTATGGCAATATCATTGTACAGAACATGTCCTTAGTAAACCGC  
A M A I S L Y R T M S L V N R 177  
586 CAGTCCTCGTCTGGGGAACATTTTTTCATGGTGGTGATCAGGTTTT  
Q S S S G E H F S 186  
631 TTGAGACTTTGCTGGCTCAATGTCGCAGGGGTTGGGGTTGGATTCT  
676 ACTTCAGCTTAATATCCTCCTCGATCCTCCTATTTTCTA

Figure 1(c)-2



(ii)

1	GGACTTCGAGGGCCATGGCATTTCACCTTGCACTTCAATACTTCA	
46	TGATCTACCAGAGGTCACGGCCCAATCATCTTTTACTGCACCACA	
	T R G H G P I I F Y C T T	13
91	ACTATTGTTGTTGTACGGTTTTACTAATAGGAGGTTGACAGGT	
	T I V V V T V L L I G G S T G	28
136	AAAATGTTGGAAGCTTTGGAAGTTGTAGGTGACGATCTTGATGAC	
	K M L E A L E V V G D D L D D	43
181	TCCATGTCTGAAGGCTTTGAAGAGAGCGATCATCAGTATGTCCCT	
	S M S E G F E E S D H Q Y V P	58
226	CCTCCTTTTAGCATTGGAGCTTCATCTGACGAGGATACATCATCA	
	P P F S I G A S S D E D T S S	73
271	TCAGGAAGCAGGTTCAAGATGAAGCTGAAGGAGTTTCACAAAACC	
	S G S R F K M K L K E F H K T	88
316	ACTACATCATTCACCGCGTTGGACAAAACTTTCTGACTCCGTTT	
	T T S F T A L D K N F L T P F	103
361	TTCACAACTAATAGTGGAGGTGGAGATGGAGATGGGGAGTAGCAT	
	F T T N S G G G D G D	114
406	GGAAAAGATGTGGAT	



Figure 1(d)-1



1 CGCCACGACCCTCAGGGCCAGGTAAAGCAGCAGCAAGCGGCCGGC  
46 GTTGGTATACTGCTTCAGATTATGATGCTCGTGCTTTCCTTCGTT  
M M L V L S F V 8  
91 CTCGGCCATGTCTCCGCCGTCATCGATTCCACTATCTTCCTGAA  
L G H V L R R H R F H Y L P E 23  
136 GCCAGCGGTTCCGTTCTCATTGGTTTAATCGTCGGTATACTTGCT  
A S G S L L I G L I V G I L A 38  
181 AATATCTCCGATACTGAGACTAGCATTAGGACGTGGTTTAATTTT  
N I S D T E T S I R T W F N F 53  
226 CACGAAGAGTTCTTCTTCTGTTTTGTTGCCTCCCATCATATTC  
H E E F F F L F L P P I I F 68  
271 CAGTCAGGTTTCAGTCTTCAACCTAAACCATTCTTTCTAACTTT  
Q S G F S L Q P K P F F S N F 83  
316 GGAGCCATTGTTACCTTTGCTATCATCGAACTTTTGTCGCTTCA  
G A I V T F A I I G T F V A S 98  
361 GTTGTACTGGTGGTCTGGTTTATCTTGGCGGCTCTATGTATCTC  
V V T G G L V Y L G G S M Y L 113  
406 ATGTATAAACTTCCCTTTGTTGAGTGTCTTATGTTTGGTGCATT  
M Y K L P F V E C L M F G A L 128  
451 ATATCAGCTACGGACCCTGTCAGTGTACTCTCTATATTCCAGGAT  
I S A T D P V T V L S I F Q D 143  
496 GTGGGCACCGATGTTAACCTGTATGCTTTGGTCTTTGGAGAAATCA  
V G T D V N L Y A L V F G E S 158  
541 GTTCTGAATGATGCTATGGCAATATCATTGTACAGAAACAATGTCC  
V L N D A M A I S L Y R T M S 173  
586 TTAGTAAACCGCCAGTCCCTCGTCTGGGGAACATTTTTTCATGGTG  
L V N R Q S S S G E H F F M V 188  
631 GTGATCAGGTTTTTTGAGACTTTTGCTGGCTCAATGCTGCAGGG  
V I R F F E T F A G S M S A G 203  
676 GTTGGGGTTGGATTCACTTCAGCTTTACTCTTTAAGTATGCAGGA  
V G V G F T S A L L F K Y A G 218  
721 TTGGACACCGAGAATCTTCAGAACTTGGAGTGTGTCTCTTTGTA  
L D T E N L Q N L E C C L F V 233  
766 CTTTCCCGTATTTTTCATACATGCTTGCAGAAGGTGTTGGTCTC  
L F P Y F S Y M L A E G V G L 248  
811 TCCGGCATTGTTTCTATACTCTTCACAGGAATTGTTATGAAGCGC  
S G I V S I L F T G I V M K R 263

Figure 1(d)-2



856 TACACTTTCTCAAATCTCTCAGAAGCTTCACAGAGTTTCGTATCT  
Y T F S N L S E A S Q S F V S 278  
901 TCTTTTTTTCACCTTGATATCTTCGCTAGCAGAACTTTCACGTTT  
S F F H L I S S L A E T F T F 293  
946 ATTTACATGGGATTGATATTGCCATGGAGCAGCATAGCTGGTCC  
I Y M G F D I A M E Q H S W S 308  
991 CATGTTGGGTTTATCCTTTTCTCTATTGTATCCTCATTTACTGAT  
H V G F I L F S I V S S F T D 323  
1036 CGTCAGTGATTGTATGCAGTGGCTGTCAATGTATTTGGGTGTGCA  
R Q 325  
1081 TATTTGGTCAACCTATTTAGACAGGAGAACCAGAAGATACCTATG  
1126 AAGCACCAAAAAGCCCTTTGGTATAGTGGACTTCGAGGGGCAATG  
1171 GCATTTGCACTTGCACTTCAATCACTTCATGATCTACCAGAGGGT  
1216 CACGGCCAAATCATCTTTACTGCAAACCACAACATATGTTGTGTG  
1261 CACGGTTTTACTAATAGGAGGTTCGACAGGTAAATGTTGGAAGC  
1306 TTTGGAAGTTGTAGGTGACGATCTTGATGACTCCATGCTGAAGG  
1351 CTTTGAAGAGAGCGATCATCAGTATGTCCCTCCTCTTTTAGCAT  
1396 TGGAGCTTCATCTGACGAGGATACATCATCATCAGGAAGCAGGTT  
1441 CAAGATGAAGCTGAAGGAGTTTACAAAACCACTACATCATTCAC  
1486 CGCGTTGGACAAAACTTTCTGACTCCGTTCTTCACAACTAATAG  
1531 TGGAGATGGAGATGGAGATGGGGAGTAGCATGGAAAAGATGTGTA  
1576 TTTGTGGTCCAGGCCAAGCTATAATTAGAGTACACATATGTCTAT  
1621 GTAAGATTAACACTGGTTGATTTTACCTCTCGCAAAATGCCCACT  
1666 ATAAAGTTGACGATTTCC

Figure 1(e)-1



1 CAGGGCCAGGTTAAGCAGCAGCAAGCGGCCGGCGTTGGTATACTG  
46 CTTCAGATTATGATGCTCGTGCTTTCCTTCGTTCTCGGCCATGTC  
M M L V L S F V L G H V 12  
91 CTCCGCGGTCATCGATTCCACTATCTTCTGAAGCAGCGGTTCTG  
L R R H R F H Y L P E A S G S 27  
136 CTTCCTATTGGTTTAATCGTCGGTATACTTGCTAATATCTCCGAT  
L L I G L I V G I L A N I S D 42  
181 ACTGAGACTAGCATTAGGACGTGGTTTAATTTCCACGAAGAGTTC  
T E T S I R T W F N F H E E F 75  
226 TTCTTCTTGTTTTGTTGCCCTCCCATCATATTCCAGTCAGGTTTC  
F T F L L P P I I F Q S G F 90  
271 AGTCTTCAACCTAAACCATTCTTTTCTAACTTTGGAGCCATTGTT  
S L Q P K P F F S N F G A I V 105  
316 ACCTTTGCTATCATCGGAACTTTTGTGCTTCAGTTGTTACTGGT  
T F A I I G T F V A S V V T G 120  
361 GGTCTGGTTTATCTTGGCGGCTCTATGTATCTCATGTATAAATT  
G L V L G G S M Y L M Y K L 135  
406 CCCTTTGTTGAGTGTCTTATGTTTGGTGCACCTATATCAGCTACG  
P F V E C L M F G A L I S A T 150  
451 GACCCGTGCTACTGTACTCTCTATATTCCAGGATGTGGGCACCGAT  
D P V T V L S I F Q D V G T D 165  
496 GTTAACCTGTATGCTTTGGTCTTTGGAGAATCAGTTCTGAATGAT  
V N L Y A L V F G E S V L N D 180  
541 GCTATGGCAATATCATTGTACAGAACAATGTCCTTAGTAAACCGC  
A M A I S L Y R T M S L V N R 195  
586 CAGTCCTCGTCTGGGGAACATTTTTTCATGGTGGTGATCAGGTTT  
Q S S S G E H F F M V V I R F 210  
631 TTTGAGACTTTTGCTGGCTCAATGTCTGCAGGGTTGGGGTTGGA  
F E T F A G S M S A G V G V G 225  
676 TTCCTTCAGCTTTAATATCCTTCTCGAATCCTCTATTTTTCTT  
F T S A L I S F L E S S I F L 240  
721 ATTAGATGTCACATGGCCAAAAATGTATTGTAATACTTAACTCA  
I R C H M A K N V L 255  
766 GAACACCTCTTTAAGTATGCAGGATTGGACACCGAGAATCTTCAG  
811 AACTTGGAGTGTGTCTCTTTGTACTTTTCCCGTATTTTTCGTAA  
856 GTAGACAAAACAACTCTCTCCTGTCTCTTCGTATTTATGACAAC  
901 ACTTCTTCCCCCTAATGTATTCTGGTTATTCTGTAAGATACATGC

Figure 1(e)-2



946 TTGCAGAAGGTGTTGGTCTCTCCGGCATTGTTTCTATACTCTTCA  
991 CAGGAATTGTAATCGCCGAGTCATTGTAGCTTTTACATCTTAGTT  
1036 GATGTTAATATCTTGGAAAGACATATTTAGGCTGCCTAATATAGT  
1081 GCTACTGTAGGTTATGAAGCGCTACACTTTTCTCAAATCTCTCAGA  
1126 AGCTTCACAGAGTTTCGTATCTTCTTTTTTTCAC TTGATATCTTC  
1171 GCTAGCAGAACTTTACGTTTACATTACATGGGATTGATATTGC  
1216 CATGGAGCAGCATAGCTGGTCCCATGTTGGGTTTATCCTTTTCTC  
1261 TATTGTATCCTCATTTACTGATCGTCAGTGATTGTATGCAGTGTT  
1306 AGTCAGTGTTGTAAATCCTTGACTTTACCTTTTGCTTCTGCGTTT  
1351 CATGACTGACATCAGTTGTTTATTGGCGTGGCTAGGTGACTAAAT  
1396 GCTTTTTTATCCTGGCTGATCGCTTCATTATCACCATTGGTTTTCG  
1441 ATTCGGATTTACCTATATGTTCTGCAATGCTTTTCTCACGCAGGG  
1486 CTGTCAATGTATTGGGTGTGCATATTTGGTCAACCTATTTAGAC  
1531 AGGAGAACCAGAAGATACCTATGAAGCACC AAAAGCCCTTTGGT  
1576 ATAGTGGACTTCGAGGGGCAATGGCATTGCACTTGCACTTCAAT  
1621 CACTTCATGATCTACCAGAGGGTCACGGCCAAATCATCTTTACTG  
1666 CAACCACAAC TATTGTTGTTGTACGGTTTTACTAATAGGAGGTT  
1711 CGACAGGTAAAA TGTGGAAGCTTTGGAAGTTGTAGGTGACGATC  
1756 TTGATGACTCCATGTCTGAAGGCTTTGAAGAGAGCGATCATCAGT  
1801 ATGTCCCTCCTCCTTTTAGCATTGGAGCTTCATCTGACGAGGATA  
1846 CATCATCATCAGGAAGCAGGTTCAAGATGAAGCTGAAGGAGTTTC  
1891 ACAAACCACTACATCATTCACCGCTTGGACAAAAC TTTCTGA  
1936 CTCCGTTCTTCACAACTAATAGTGGAGATGGAGATGGAGATGGGG  
1981 AGTAGCATGGA AAAGATGTGTATTTGTGGTCCAGGCCAAGCTATA  
2026 ATTAGAGTACACATATGTCTATGTAAAGATTAACACTGGTTGATTT  
2071 TACCTCTCGCAAAATGCCCACTATAAAGTTGACGATTTCCAAGAC  
2116 ATTTCGA



Figure 2(a)-1

ANHXI	15	VS	KLP	SLS	TS
ScNHX	37	DE	LPS	DP	LP
H <sub>2</sub> NHE6	40	L	AVG	V	FWA
C <sub>2</sub> NHE1	16	FF	MS	Q	F
ANHXI	29	---	---	---	---
ScNHX	70	SW	AL	FW	AL
H <sub>2</sub> NHE6	80	SAN	LL	FW	LL
C <sub>2</sub> NHE1	31	---	---	---	---
ANHXI	66	LG	GT	VT	LL
ScNHX	110	V	IG	L	IR
H <sub>2</sub> NHE6	120	L	VGL	Y	IR
C <sub>2</sub> NHE1	58	UE	GF	F	AD
ANHXI	90	LF	FI	LL	PP
ScNHX	133	YF	FN	LL	PP
H <sub>2</sub> NHE6	159	VF	FN	LL	PP
C <sub>2</sub> NHE1	83	VF	FN	LL	PP
ANHXI	130	SC	TI	IS	LG
ScNHX	173	SA	VV	IG	IL
H <sub>2</sub> NHE6	199	SC	FI	GS	IM
C <sub>2</sub> NHE1	123	SC	FI	GS	IM
ANHXI	165	TD	SV	CT	LQ
ScNHX	209	TD	PT	IL	IS
H <sub>2</sub> NHE6	239	TD	PT	VL	LA
C <sub>2</sub> NHE1	157	TD	PT	IL	IS
ANHXI	201	IQ	SF	DL	---
ScNHX	246	CQ	KH	GG	---
H <sub>2</sub> NHE6	279	TV	AY	QP	AG
C <sub>2</sub> NHE1	194	JE	FN	FS	---



Figure 2(a)-2

ANHX1	239	GLTSAVYIKK	LSGILTVFEC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC
SCNX1	284	GILVALLLDKH	MSGJVSLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
HNHE6	319	GVVITALLTKF	FTGVNAVLLFC	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
CNHE1	234	GCMNAFLITKM	LTGTINSVLF	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
ANHX1	279	LSGILTVFEC	MSGJVSLLFC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC
SCNX1	323	MSGJVSLLFC	FTGVNAVLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
HNHE6	358	FTGVNAVLLFC	LTGTINSVLF	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
CNHE1	273	LTGTINSVLF	MSGJVSLLFC	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
ANHX1	319	AEITFIIFYVG	MSGJVSLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
SCNX1	363	SENFIFIVLGG	FTGVNAVLLFC	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
HNHE6	398	AENFIFISYMG	LTGTINSVLF	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
CNHE1	313	MESFIFCYIG	MSGJVSLLFC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC
ANHX1	359	MVGRAAFVFP	MSGJVSLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
SCNX1	396	CVIARWCAYFP	FTGVNAVLLFC	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
HNHE6	431	FLGRAANTYFP	LTGTINSVLF	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
CNHE1	346	TASRALFVFP	MSGJVSLLFC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC
ANHX1	384	INFMQVTVW	MSGJVSLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
SCNX1	436	IPYNYQMMTF	FTGVNAVLLFC	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
HNHE6	453	IGSNFOHMM	LTGTINSVLF	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
CNHE1	368	IPKRYQHMMJL	MSGJVSLLFC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC
ANHX1	424	IMITSTITVC	MSGJVSLLFC	SENFIFIVLGG	363	CVIARWCAYFP	436	IPYNYQMMTF	468	TLLATVTVV
SCNX1	468	TLLATVTVV	FTGVNAVLLFC	AENFIFISYMG	398	FLGRAANTYFP	453	IGSNFOHMM	486	MMFSTITLLV
HNHE6	486	MMFSTITLLV	LTGTINSVLF	MESFIFCYIG	313	TASRALFVFP	346	IPKRYQHMMJL	401	MJFAITTA
CNHE1	401	MJFAITTA	MSGJVSLLFC	AEITFIIFYVG	319	MVGRAAFVFP	384	INFMQVTVW	424	IMITSTITVC



Figure 2(a)-3

ANHX1	TLFSTVVFGL	TKPLTISYLLP	HONATISMLS	D---	D	TPKS	461
SCNX1	VLTVLIFGGT	IAGMLEVLNT	KITCISEEDT	S---	D	DEFD	504
HNHE6	FFTVWVGGG	TTAMLSCLHI	RIVGVDSQEH	LGVP	EN	ERRIT	526
CNHE1	TIVTVLVNGGL	TSWMIDYLQII	KHGGKDAHEEG	Q-R	LEN	SMS	440
ANHX1	IHIP-----	-----L	DSFIEPSG	-----	-----	-----	477
SCNX1	IEAP-----	-----R	STOTDLG	-----	-----	-----	525
HNHE6	TKAESAWLFR	MWYNFDHNYL	KPULLTHSGPP	LTTTL	P	ACCG	566
CNHE1	SPAD-----	-----Q	HSDEDES	VPVT	MSP	G	462
ANHX1	-NHNVPRPDS	IRGFLTRPTR	TVHYVWRQFD	DS	FMRP	VFGG	516
SCNX1	YSDNNSPDIS	IDQFAVSSNK	NLPNNJTSITG	GN	T	FGLNET	565
HNHE6	PIARCLTSPQ	AYENOEQLKD	DDSLLJLNDG	D	S	LTYGDS	606
CNHE1	PWDKAFLPK	WYHEDAEWQL	LK-LV	FQFH	ET	STDPDAI	500
ANHX1	RGFVFPVGS	PTERNPPDLS	KA-----	-----	-----	-----	538
SCNX1	ENTSPNARS	SMOKRNLRDK	LGTFINSDSQ	WFQNF	DEQVL	-----	605
HNHE6	VNTEPATSSA	PRFRMGNSSE	DALDRELAFG	DHEL	VIRGTR	-----	646
CNHE1	FGTINTPTVLS	SIDFLVDFKP	STRVRQCRAL	QYNCT	IRDSI	-----	540
ANHX1	-----	-----	-----	-----	-----	-----	538
SCNX1	KPVFLDNVSP	SLQDSATQSP	ADFS	SSQN	H	-----	633
HNHE6	LVLPMDDESEP	PLNLLDNTRH	GPA	-----	669	-----	669
CNHE1	D-----	-----	-----	-----	-----	-----	541

Figure 2(b)-1

ANHX1	M L D S L V S K L P	S I L S T S D H A S V	V A L N L F V A L L	C A C I V L G H L L	40
ANHX2	W S I G L T E F V T	N K L A A E H P Q V	U P I S V F I A L L	C C L V L G H L L	40
ANHX3	---	---	-----NMML	V L S F L G H V L	13
ANHX1	E E N R - - W M N E	S I T A L L I G L G	T G V T L L L I S K	G K S S - H L C V F	77
ANHX2	E E N R - - W Y N E	S I T A L L V G A A	S G T V L L L I S K	G K S S - H L C V F	77
ANHX3	R R H R F H Y L P E	A S G S L L I G L I	V G I L A N I S D T	E T S I R I W F N E	53
ANHX1	S E D L F F Y L L L	P P I I F N A G F Q	V K K K Q F F R N F	V T I M L F G A V G	117
ANHX2	D E E L F F Y L L L	P P I I F N A G F Q	V K K K K F F H N F	L T I M S F G V I G	117
ANHX3	H E E F F E F L L	P P I I F Q S G F S	L Q P K P F F S N F	G A I V F E A L I G	93
ANHX1	T I I S C T I I S L	G V T Q F F K K L D	I G T F D L G D Y L	A I G A I E A A T D	157
ANHX2	V F I S T V I I S F	G T W W L F P K I G	F K G I S A R D Y L	A I G T I E S S T D	157
ANHX3	T F V A S V Y T G G	L V Y L G G S M Y L	M A Y K L P F V E C L	M F G A L I S A T D	133
ANHX1	S V C T L Q V I N Q	D E T P L - L Y S L	V F G E G V V N D A	T S V V V F N A I Q	196
ANHX2	T V C T L Q I L H Q	D E T P L - L Y S L	V F G E G V V N D A	T S V V V F N A V Q	196
ANHX3	P V T V L S I F Q D	V G T D V N L Y A L	V F G E S V L N D A	M A I S L Y R T M S	173
ANHX1	S F I D L T H N H E	A A F H L L G N F L	Y L F L L S T L L G	A A T G L I S A Y V	236
ANHX2	K I O F E S L T G W	T A L Q V F G N F L	Y L F S T S T L L G	I G V G L L T S F V	236
ANHX3	L V N R Q S S S G E	H F F M V I T R F F	E T H A G S M S A G	V G V G F T S A L L	213
ANHX1	T K K L Y F G - R H	S T D R E V A L M M	L M A Y L S Y M L A	E L F D L S G I L T	275
ANHX2	L K T L Y F G - R H	S T T R E L A I M V	L M A Y L S Y M L A	E L F S L S G I L T	275
ANHX3	F K Y A G L D T E N	L Q N L E C C L F V	L F P Y F S Y M L A	E G V G L S G I V S	253







Figure 2(b)-2

ANHX1	VFECGIVMSH	YTWNVTESS	RITTRKHTFAT	LSFLAETFFIF	315
ANHX2	VFECGVLMSH	YASVYNVTESS	RITSRHVFAM	LSFLAETFFIF	315
ANHX3	VFETGIVMKR	YTESNLSBAS	QSFVSSFHLL	LSFLAETFFIF	293
ANHX1	LYVGMQ-ALD	IDKMRSSVSDT	PGTSTAVSSJ	LMGLVMVGRA	354
ANHX2	LYVGTD-ALD	FTKWKTSLSLS	FGGTLGVSGW	ITALLVLLGRA	354
ANHX3	LYMGFDIAME	QHSWSHVG--	FILFSIVSSF	TDQR-----	325
ANHX1	AFVEFPLSFLS	NLAKKNQ--S	EKINFNMQVV	IWWSGLMRGA	392
ANHX2	AFVEFPLSVLT	NFMNRHTERN	ESI TEKHQVI	IWWAGLMRGA	394
ANHX3	-----	-----	-----	-----	325
ANHX1	VSMALAYNKF	TRAGHLDVRG	NAIMTTSTIT	VCLFSTVVFG	432
ANHX2	VSIALAFKQF	TVSGVLLDPV	NAAMVTNTTI	VVLFITLLVFG	434
ANHX3	-----	-----	-----	-----	325
ANHX1	MLTKPLISYL	LPHQNAITTSM	LSDDNTPKSI	HIP--LLDQD	470
ANHX2	FLTKPLVNYL	LPQDASHNTG	NRGKRTEPGS	PKEDATLPLL	474
ANHX3	-----	-----	-----	-----	325
ANHX1	SFJEPSSGNHN	VPRPDSIRGFG	LTRPRTIRVHY	YWRQFDDSFM	510
ANHX2	SEDESAS TNF	NRARDSLSLL	MEQPVYTIHR	YWRKEDDTYM	514
ANHX3	-----	-----	-----	-----	325
ANHX1	RPVFGGRGFV	PFVPGSPTER	NPPDLSKA	-----	538
ANHX2	RPVFGGPRRE	NQPEC-----	-----	-----	529
ANHX3	-----	-----	-----	-----	325



Figure 2(c)

ANHX ANHX4	MMLVLSFVLG MMLVLSFVLG	HVLRRRHRFH HVLRRRHRFH	LPEASGSLI LPEASGSLI	GLIVGILAN GLIVGILAN	40 40
ANHX ANHX4	SDTETSIRTW SDTETSIRTW	ENFHEEFFFL ENFHEEFFFL	FLPPILFQS FLPPILFQS	GFSLOPKPEF GFSLOPKPEF	80 80
ANHX ANHX4	SNFGAIVTFA SNFGAIVTFA	IIGTFVASVV IIGTFVASVV	TGGLVYLGGS TGGLVYLGGS	MYLNYKLPEV MYLNYKLPEV	120 120
ANHX ANHX4	ECLMFGALIS ECLMFGALIS	ATDPVTVLSI ATDPVTVLSI	FQDVGTDVNL FQDVGTDVNL	YALVFGEVSL YALVFGEVSL	160 160
ANHX ANHX4	NDAMATSLYR NDAMATSLYR	TMSLVNRQSS TMSLVNRQSS	SGEHFFMVVI SGEHFFMVVI	RFETTFAGSM RFETTFAGSM	200 200
ANHX ANHX4	SAGVGVGFTS SAGVGVGFTS	ALIFKYAGLD ALISFLESSI	TENLQNTDEC FLIRCHMAKN	LFVLPYFSY VL-----	240 232
ANHX ANHX4	MLAEGVGLSG -----	IVSILFTGIV -----	MKRYTFSNLS -----	EASQSFVSSF -----	280 232
ANHX ANHX4	FHLISSLAET -----	FTFIYMGFDI -----	AMEQHSWSHV -----	GFILFSIVSS -----	320 232
ANHX ANHX4	FTDRQ -----	325 -----	-----	-----	232

Figure 5(a)-1



ATGTTGGATTCTCTAGTGTGCGAACTGCCTTCGTTATCGACATCTGATCAC  
GCTTCTGTGGTTGCGTTGAATCTCTTTGTTGCACTTCTTTGTGCTTGTATT  
GTTCTTGGTCATCTTTTGAAGAGAATAGATGGATGAACGAATCCATCACC  
GCCTTGTGATTGGGCTAGGCACCTGGTGTACCATTGTGTTGATTAGTAAA  
GGAAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGATCTTTTCTTCATATAT  
CTTTTGCCACCCATTATATTCAATGCAGGGTTTCAAGTAAAAAAGAAGCAG  
TTTTTCCGCAATTCGTGACTATTATGCTTTTGGTGTCTGTTGGGACTATT  
ATTTCTTGCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAAGAAGTTG  
GACATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTT  
GCTGCAACAGATTACAGTATGTACACTGCAGGTTCTGAAATCAAGACGAGACA  
CCTTTGCTTTTACAGTCTTGATTTCGGAGAGGGTGTGTGAATGATGCAACG  
TCAGTTGTGGTCTTCAACGCGATTACAGAGCTTTGATCTCACTACCTAAAC  
CACGAAGCTGCTTTTTCATCTTCTTGAAACTTCTTGATTTTGTTCCTTA  
AGTACCTTGCTTGGTGCTGCAACCGGTCTGATAAGTGCGTATGTTATCAAG  
AAGCTATACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATG  
CTTATGGCGTATCTTTCTTATATGCTTGCTGAGCTTTTCGACTTGAGCGGT  
ATCCTCACTGTGTTTTTCTGTGGTATTGTGATGTCCATTACACATGGCAC  
AATGTAACGGAGAGCTCAAGAATAACAACAAAGCATACCTTTGCAACTTTG  
TCATTTCTTGCGGAGACATTTATTTCTTGATGTTGGAATGGATGCCTTG  
GACATTGACAAGTGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA  
GTGAGTCAATCCTAATGGGTCTGGTCATGGTTGGAAGAGCAGCGTTTCGTC  
TTTCCGTTATCGTTTCTATCTAACTTAGCCAAGAAGAATCAAAGCGAGAAA  
ATCAACTTTAACATGCAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGT  
GCTGTATCTATGGCTCTTGCAACAACAAGTTTACAAGGGCCGGGCACACA  
GATGTACGCGGGAATGCAATCATGATCACGAGTACGATAACTGTCTGTCTT  
TTTAGCACAGTGGTGTGGTATGCTGACCAAAACCACTCATAAGCTACCTA  
TTACCGCACCAGAACGCCACCACGAGCATGTTATCTGATGACAAACCCCCA  
AAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTCATTGAGCCTTCA  
GGGAACCACAATGTGCCTCGGCCGTGACAGTATACGTGGCTTCTTGACACGG  
CCCACTCGGAACCGTGCACTACTAACTGGAGACAATTTGATGACTCTTTCA  
TGCACCCGTCTTTGGAGGTGCTGGCTTTGTACCCTTTGTTCCAGGTTCTC  
CAACTGAGAGAAACCCCTCTGATCTTAGTAAGGCTTGAGGGTAACGTGGAA  
GAAAAGCTTTGATTTTTTTTTGGTAGAAAAGGGTGATTCAAATTATGCTTTT  
GTGTAATTATCCATTTGTAATATGTTTGTGAGGACAGAAATCTGTCCTA  
ACGTTTTGAGAGCAGAAAGCAAAACATGGCAACTTTGAAGTGTTTGATTGA  
TGTATGTAATTATATTCATATTTGTTTGTGTAACACAAACTACACTTTT  
GTTTATGTTTTGAATTTGGTTTTTGTCTCGAAAAA

Figure 5(a)-2



MLDSLVS KLPSLSTSDHASVVALNLFVALLCACIVLGHLEENRWMNESIT  
ALLIGLGTGV TILLISKGKSSHLLVFESEDLFFIYLLPPIIFNAGFQVKKKQ  
FFRNFTVIMLFGAVGTIISCTIISLGVTQFFKKLDIGTFDLGDYLAIGAIF  
AATDSVCTLQVLNQDETPLYSLVFGEGVNDATSVVVFNAIQSFDLTHLN  
HEAAFHLLGNFLYLFLLLSTLLGAATGLISAYVIKKLYFGRHSTDREVALMM  
LMAYLSYMLAEFLDLSGILTVFFCGIVMSHYTWHNVTESSRITTKHTFATL  
SFLAETFI FLYVGM DALDIDK WRSVSDTPGTSIAVSSILMGLVMVGRAAFV  
FPLSFLSNLAKKNQSEKINFNMQVVIIWWSGLMRGAVSMALAYNKFTRAGHT  
DVRGNAIMITSTITVCLFSTVVFGMLTKPLISYLLPHQNATTSMLSDDNTP  
KSIHIPLLDQDSFIEPSGNHNVPRPDSIRGFLTRPTRNRALLTGDNLM TLS  
CDPSLEVVALYPLFQVLQRETLLILVRLEGNVEEKL

Figure 5(b)-1



1	TTCGCGGCCGCGTCTCTCTCTATTTCCAGTAAAAATCGAAATTC	
47	GTATAATTTCCCTCAGTCCCGTAATTTTCTCCTTTTTTTTCTTCCC	
92	CAATTCCTTCAATTTTCGAATTCGCTCTCTGTTTCGTTCCCTCGT	
137	AGACGAAGAAGAAGAAGAAATCTCAGGTTTTAGCTTTCGAAGCTTC	
182	CAAAATTTTGAATTTTGATCTTCTGGGCTCTTTGTAAATCAGAC	
227	TGAAGATATTTAGATTACCCAGAAGTTGTTCAAGGAATGGTTTCA	
272	GTGGACAGCACGGAAAGATAAAAGAGACTTTTTTTTCCAGATTTT	
317	GCTGATCCAAAATCTGAATAGTTGTTTCATGTTCTTGGATCAAATC	
362	TGAAAAGAGGAAGTTTGTGGATCTAGAAGAAGATAACAATGTTG	
	M L	2
407	GATTCTCTAGTGTGAAACTGCCTTCGTTATCGACATCTGATCAC	
	D S L V S K L P S L S T S D H	17
452	GCTTCTGTGGTTGCGTTGAATCTCTTTGTTGCACTTCTTTGTGCT	
	A S V A L N L F V A L L C A	32
497	TGTATTGTTCTTGCTCATCTTTTGGAAAGAGATAGATGGATGAAC	
	C I V L G H L L E E N R W M N	47
542	GAATCCATCACGCGCTTGTGATTGGGCTAGGCACTGGTGTTACC	
	E S I T A L L I G L G T G V T	62
587	ATTTGTTGATTAGTAAAGGAAAAAGCTCGCATCTTCTCGTCTTT	
	I L L I S K G K S S H L L V F	77
632	AGTGAAGATCTTTTCTTCATATATCTTTTGCCACCCATTATATTC	
	S E D L F F I Y L L P P I I F	92
677	AATGCAAGGTTTCAAGTAAAAAAGAAGCAGTTTTCGCAATTTTC	
	N A G F Q V K K K Q F F R N F	107
722	GTGACTATTATGCTTTTTTGGTGCTGTTGGGACTATTATTCTTTCG	
	V T I M L F G A V G T I I S C	122
767	ACAATCATATCTCTAGGTGTAACACAGTTCCTTAAAGAAGTTGGAC	
	T I I S L G V T Q F F K K L D	137
812	ATTGGAACCTTTGACTTGGGTGATTATCTTGCTATTGGTGCCATA	
	I G T F D L G D Y L A I G A I	152
857	TTTGCTGCAACAGATTTCAGTATGTACACTGCAGGTTCTGAATCAA	
	F A A T D S V C T L Q V L N Q	167
902	GACGAGACACCTTTGCTTTACAGTCTTGATTCGGAGAGGGTGGT	
	D E T P L L Y S L V F G E G V	182
947	GTGAATGATGCAACGTCAGTTGTGGTCTTCAACGCGATTACAGAC	
	V N D A T S V V V F N A I Q S	197

Figure 5(b)-2

992 TTTGATCTCACTCACCTAAACCACGAAGCTGCTTTTCATCTTCTT  
F D L T H L N H E A A F H L L 212  
1037 GGAAACTTCTTGATTTGTTTCTCCTAAGTACCTTGCTTGGTGT  
G N F L Y L F L L S T L L G A 227  
1082 GCAACCGTCTGATAAGTGCCTATGTTATCAAGAAGCTATACTTT  
A T G L I S A Y V I K K L Y F 242  
1127 GGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATG  
G R H S T D R E V A L M M L M 257  
1172 GCGTATCTTTCTTATATGCTTGCTGAGCTTTTCGACTTGAGCGGT  
A Y L S Y M L A E L F D L S G 272  
1217 ATCCTCACTGTGTTTTTCTGTGGTATTGTGATGTCCATTACACA  
I L T V F F C G I V M S H Y T 287  
1262 TGGCACAATGTAACGGAGAGCTCAAGAATAACAACAAGCATACC  
W H N V T E S S R I T T K H T 302  
1307 TTTGCAACTTTGTCTATTCTTGCGGAGACATTTATTTCTTGAT  
F A T L S F L A E T F I F L Y 317  
1352 GTTGAATGGATGCCTTGACATTGACAAGTGAGATCCGTGAGT  
V G M D A L D I D K W R S V S 332  
1397 GACACACCGGGAACATCGATCGCAGTGAGCTCAATCCTAATGGGT  
D T P G T S I A V S S I L M G 347  
1442 CTGGTCATGGTTGGAAGAGCAGCGTTCGTCTTTCCGTTATCGTTT  
L V M V G R A A F V F P L S F 362  
1487 CTATCTAACTTAGCCAAGAAGAAATCAAAGCGAGAAAAATCAACTTT  
L S N L A K K N Q S E K I N F 377  
1532 AACATGACGGTTGTGATTGGTGGTCTGATGAGAGGTGCT  
N M Q V V I W W S G L M R G A 392  
1577 GTATCTATGGCTCTTGATACACAAGTTTACAAGGGCCGGGCAC  
V S M A L A Y N K F T R A G H 407  
1622 ACAGATGTACGCGGAATGCAATCATGATCAGAGTACGATAACT  
T D V R G N A I M I T S T I T 422  
1667 GTCTGTCTTTTTAGCACAGTGGTGTGGTATGCTGACCAAACCA  
V C L F S T V V F G M L T K P 437  
1712 CTCATAAGCTACCTATTACCGCACCAGAACGCCACCACGAGCATG  
L I S L L P H Q N A T T S M 452  
1757 TTATCTGATGACAACACCCCAAAATCCATACATATCCCTTTGTTG  
L S D D N T P K S I H I P L L 467



Figure 5(b)-3

1802 GACCAAGACTCGTTCATTGAGCCTTCAGGGAACCACAATGTGCCT 482  
D Q D S F I E P S G N H N V P  
1847 CGGCTGACAGTATACGTGGCTTCTTGACACGGCCCACTCGGAAC 497  
R P D S I R G F L T R P T R N  
1892 CGTGCATTACTAACTGGAGACAATTTGATGACTCTTTCATGCGAC 512  
R A L L T G D N L M T L S C D  
1937 CCGTCTTTGGAGGTCGTGGCTTTGTACCCTTTGTTCAGGTTCTC 527  
P S L E V V A L Y P L F Q V L  
1982 CAACTGAGAGAAACCCTCCTGATCTTAGTAAGGCTTGAGGGTAAC 542  
Q L R E T L L I L V R L E G N  
2027 GTGGAAGAAAAGCTTTGA 547  
V E E K L



Figure 8 (a)

[SEQ ID NO:21]

1 mpdskhwil lfrdgdddd ddgqdpalqe lysswalfil lvlligallt  
51 syyvqskkir aihetvisvf vgmvvgliir vspgliiqnm vsfhstyffn  
101 vllppiilns gyelhqsnff rnigtltfa fagtffisavt lgvlvyifsf  
151 lnfenlsmtf vealsmgatl satdpvtvla ifnsykvdkk lytiifgesi  
201 lndavaivmf etlqqfggkt lhfftlfsgf gifiitffis lligvsgigli  
251 talllkysyl rrypsiesci illmaytsyf fsngchmsgv vsllfcgiti  
301 khyaffrmsy kaklstkyvf rvlaqlsenf ifiylgmslf tqvdlvykpi  
351 filittvavt asrymnvflpl snllnkfhrq rngnlidhip ysyqmmfwa  
401 glrgavgval aagfegenag tlrattlvvv vltliifggt tamleilhi  
451 etgvaadvds dteigmlpwq qspefdlens amelsdasae pvvvdqqftt  
501 ehfdegniap tskkvsstf eqyqraagaf nqffhssrdd gaqwltrfde  
551 evikpvller dnlkngtkk





Figure 8 (b)

[SEQ ID NO:22]

1 mlskvllnia fkvllttakr avdpdddel lpsdpdpdgsd dpiagdppdvd  
51 lnpvteemfs swalfimlll lsalwssyy ltqkriravh etvlsifygm  
101 vigliirmsp ghyiqdvtvf nssyffnvl ppiilnsge lnqvnffnm  
151 lsilifaipg tfisavvigi ilyiwtflgl esidisfada msvgatlsat  
201 dpvtilsifn aykvdpklyt iifgesllnd aisivmfetc qkfhgqpatf  
251 ssvfegaglf lmtfsvslli gvliliglval llkhthirry pqiesclill  
301 iayesyffsn gchmsgivsl lfcgitlkhy aaynmsrrsq itikyifqll  
351 arlsenfifi ylglelftv elvykpllii vaaisicvar wcavfplsqr  
401 vniwyrvkti rsmggitgen isvpdeipyn yqmmtfwagl rgavgvalal  
451 giggeykftl latvlvvvl tviifggta gmlevlnikt gciseedtsd  
501 defdieapra inllngssiq tdlgpysdnn spdisidqfa vssknklnpn  
551 isttgntfng glnetentsp nparssmdkr nlrcklgtif nsdsqwfqnf  
601 deqvlkpvl dnvspslqds atqspadfss qnh



### Figure 8 (c)

[SEQ ID NO:23]

1 caagaagcta tacattggaa ggcattctac tgaccgtgag gttgccctta  
51 tgatgctcat ggcttacctt tcatatatgc tggctgagtt gctagatttg  
101 agcggcattc tcaccgtatt cttctgtggt attgtaatgt cacattacac  
151 ttggcataac gtcacagaga gttcaagagt tacaacaaag cagcgatttg  
201 caactctgtc cttcattgct gagacttttc tcttctctga tgttgggatg  
251 gatgcattgg atattgaaaa atgggagantt nccagtgaca gacctggnaa  
301 atccattngg gtaagctcaa ttttgctagg gattgggtcc tgattggaag  
351 ngctgctttt gnaattcccc tggtggtc

### Figure 8 (d)

[SEQ ID NO:24]

1 gtttggtaat tggaggaggt ggagtaatgg agctcgggtt ggggatgggg  
51 atggggcttg gcgacccgnc tgcggactac ggctcgatcg cggcgggtgg  
101 gatgttcgtg gcgctcatct gcgtctgcat cgctgctggc cacctcctcg  
151 aggagagccg atggatgaac gagtccatca ccgcgctaata catcgggttg  
201 ggtacttgga ggagtgnntt tgnatggtgt cgagctggaa gcaactcgna  
251 tactggtgtt cagcgagg



### Figure 8 (e)

[SEQ ID NO:25]

1 acattccctg aaagnaactgc tggacntttg agggctcgga tgcctgtaga  
51 tccaggactc aaaggatgnt gagctagagg ttgttgggat ggtgaagttt  
101 gcttaccaag ggccatttac attgtctggc atcaaaactat gccagccac  
151 tgatggcacg gctcagttta atgaggtctg ccacaccttc tccagtggga  
201 gttatctgtg catctaattg gtacctcttt tgtattgtag ttgttacttt  
251 acccttgatt tgttcggttt gcttctaaag caggttgtga aattcctatt  
301 gtatgtngtg acgcttggtt gttttttgag gctggaaatt acatcatggt  
351 ttgtatttgt ctattaaaaa aaaaaaaaaa

### Figure 8 (f)

[SEQ ID NO:26]

1 gtcaaaaactc atccctcctc ttccatttgc atattctctt ttatcatctt  
51 ttcttcctta aattagagtc tacccttcg cccatagtct ttgacaccct  
101 ttcaaaaatt ctagaacaag aattttattc ttcatatata tatatatata  
151 tatccaatta accatctcaa tctcatattc acatatacct cataaaccat  
201 ccataacatc cttaaaaacc ctctaagccc ttcaaaactt tgatttgtaa  
251 ttgtttctct tataagtctt aacctgcaca aatcaatttt aatttcttat  
301 gttcatatag ttatgaatga ttgaaaaaaa cacaatgac tccagttatc  
351 tgtgagatct ctatgataaa ctctactctc cagacgcagg acacatttag  
401 ttcaatcttt ctctgttgtt ttctctact ggttctatat ttctcatga  
451 attattaatt aatcctatat tctttctttt caatacaaat ttagtttcat  
501 taattctatc aacataatca attaaactac atagttagaa aaatagtact  
551 attaccacga tcaactcaaag ttttttagtt ttaacaacac antctg



## Figure 8 (g)

[SEQ ID NO:27]

1 atttaccatgg ttataccagt tatcttgagc acttatgcat catccagtga  
51 tcagttttgc ttccattcag actgatgggt ctggcagaag taatgtattc  
101 tgggtggactt acatctatca gcgatgatga aacttgatga tcagtttttt  
151 tagttgaaaa attctgcaag aacagctact taatgtctta ttgtgtatcg  
201 caggcacaca tcagctgctg atgtctgcta tacttctgta ctctcactat  
251 agctcatcta tgacgtctag acatgctagc gtatgtgtan nnnacatcgc  
301 gctagtatgt ataactctcac atcatatgct actgttctat atagaactat  
351 gtgatagcta ctgtatact gctgtcatac agagtcccg taatatcaat  
401 gctattttgc tttctcaaa gaaaaaagga aatgactttc cttttgatta  
451 tatatttgat ccagggtttc ggcttgctga ctaagcctct gattaatctc  
501 ctctgtccac caagacctgg ca

## Figure 8 (h)

[SEQ ID NO:28]

1 ttcccgttat cgtttctatc taacttagcc aagaagaatc aaagcgagaa  
51 aatcaacttt aacatgcagg ttgtgatttg gtggctcgtt ctcatgagag  
101 gtgctgtatc tatggctctt gcatacaaca agtttacaag ggccgggac  
151 acagatgtac gngggaatgc aatcatgac acngtacgn taactgtctg  
201 tnttttttag acagtgggtt ttggtagct gaccaaacca ntcataagct  
251 acctatttac cgnaccanga accgtcatca acnggcatg tttatcttgn  
301 atncaataa acccnaanaa tcnataacca

